

#14



1 (1) GENERAL INFORMATION:

2 (i) APPLICANTS: Boon, Thierry, Van den Eynde, Beno t

3 (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
4 Rejection Antigens and Uses Thereof

5 (iii) NUMBER OF SEQUENCES: 16

6 (iv) CORRESPONDENCE ADDRESS:

7 (A) ADDRESSEE: Felfe & Lynch
8 (B) STREET: 805 Third Avenue
9 (C) CITY: New York City
10 (D) STATE: New York
11 (F) ZIP: 10022

12 (v) COMPUTER READABLE FORM:

13 (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
14 (B) COMPUTER: IBM
15 (C) OPERATING SYSTEM: PC-DOS
16 (D) SOFTWARE: Wordperfect

17 (vi) CURRENT APPLICATION DATA:

18 (A) APPLICATION NUMBER: 07/807,043
19 (B) FILING DATE: 12-DECEMBER-1991
20 (C) CLASSIFICATION:

21 (vii) PRIOR APPLICATION DATA:

22 (A) APPLICATION NUMBER: 07/764,364
23 (B) FILING DATE: 23-SEPTEMBER-1991

24 (viii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: 07/728,838
26 (B) FILING DATE: 9-JULY-1991

27 (ix) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: 07/705,702
29 (B) FILING DATE: 23-May-1991

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: Hanson, Norman D.
32 (B) REGISTRATION NUMBER: 30,946
33 (C) REFERENCE/DOCKET NUMBER: LUD 253.3

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: (212) 688-9200
36 (B) TELEFAX: (212) 838-3884

37 (2) INFORMATION FOR SEQUENCE ID NO: 1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 462 base pairs
40 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: singular
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: genomic DNA
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58
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61
62 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
63 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCACTCCCT CAGCCAATGA GCTTACTGTT 120
64 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTGCA AGTTCCGCCT ACAGCTCTAG 180
65 CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
66 CCCCTCTCCA CCTCGTGTCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
67 AGAACTCTTC CGGAGGAAGG AGGGAGGACCC CCCCCCTTTT GCTCTCCAG CATGCATTGT 360
68 GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
69 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTGTG CC 462
70
71 (2) INFORMATION FOR SEQUENCE ID NO: 2:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 675 base pairs
74 (B) TYPE: nucleic acid
75 (C) STRANDEDNESS: singular
76 (D) TOPOLOGY: linear
77 (ii) MOLECULE TYPE: genomic DNA
78 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
79
80
81
82 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
83 Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
84 5 10 15
85
86 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
87 Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
88 20 25 30
89
90 GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
91 Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
92 35 40 45
93
94 AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
95 Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
96 50 55 60
97
98 TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
99 Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
100 65 70 75 80
101
102 TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
103 Ser Val Asp Glu Asp Asp Asp Glu Asp Asp Asp Glu Asp Asp Tyr Tyr
104 85 90 95
105
106 GAC GAC GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336

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107 Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
108 100 105 110
109
110 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
111 Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
112 115 120 125
113
114 GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432
115 Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
116 130 135 140
117
118 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
119 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
120 145 150 155 160
121
122 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
123 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
124 165 170 175
125
126 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
127 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
128 180 185 190
129
130 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG 624
131 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu
132 195 200 205
133
134 GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
135 Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
136 210 215 220 225
137
138 TAG 675
139
140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
141 (i) SEQUENCE CHARACTERISTICS:
142 (A) LENGTH: 228 base pairs
143 (B) TYPE: nucleic acid
144 (C) STRANDEDNESS: singular
145 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: genomic DNA
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
148
149
150
151
152 GCATGCAGTT GCAAAGCCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
153 TTCCCCCTTCA TTAATTTCT AGTTTTAGT AATCCAGAAA ATTTGATTGTT GTTCTAAAGT 120
154 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
155 ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTGAC TTGCATAC 228
156
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159 (2) INFORMATION FOR SEQUENCE ID NO: 4:

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160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 1365 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: singular
164 (D) TOPOLOGY: linear
165 (ii) MOLECULE TYPE: genomic DNA
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
167
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171 ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
172 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTCGCAT ATTCACTCCCT 100
173 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
174 AAGTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT 200
175 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCTCCA 250
176 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
177 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCAG 350
178 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
179 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
180 ACCCTTTGTG CC 462
181 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
182 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
183 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
184 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
185 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
186 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
187 GAT GAA GAC GAT GAG GAT GAT GAC TAC TAC GAC GAC 756
188 GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
189 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
190 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
191 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
192 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
193 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
194 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
195 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
196 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
197 TAG 1137
198 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
199 TTGTTTTTTT TTCCCTTCA TTAATTTCCT AGTTTTAGT AATCCAGAAA 1237
200 ATTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
201 CTGACTGCAT GGTGAACCTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
202 GTTAAAAATA AAAGTTGAC TTGCATAC 1365
203
204
205
206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
207 (i) SEQUENCE CHARACTERISTICS:
208 (A) LENGTH: 4698 base pairs
209 (B) TYPE: nucleic acid
210 (C) STRANDEDNESS: singular
211 (D) TOPOLOGY: linear
212 (ii) MOLECULE TYPE: genomic DNA

213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

214		
215		
216		
217	ACACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
218	GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCACTCCT	100
219	CAGCCAATGA GCTTACTGTT CTCGTGGGG GTTTGTGAGC CTTGGGTAGG	150
220	AAGTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCCTT	200
221	CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCCTCCA	250
222	CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCGGTAT	300
223	AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTT GCTCTCCCAG	350
224	CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
225	CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
226	ACCTTTGTG CC	462
227	ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
228	GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
229	TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
230	TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
231	ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
232	TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
233	GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC	756
234	GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
235	GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
236	GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
237	GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T	916
238	GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGGGGGT GCATTCTTA	966
239	CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC	1016
240	TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC	1066
241	CCCCCACTCCT TGCTCCGCTC TCTTTCCCTT TCCCCACCTTG CCTCTGGAGC	1116
242	TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC	1166
243	TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCCTC	1216
244	TTCAGGCTTC CCCATTGCT CCTCTCCCGA AACCCCTCCCC TTCTGTTC	1266
245	CCTTTTCGCG CCTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT	1316
246	TCACCAAGCTT TGCTCTCCCT GCTCCCCCTCC CCCTTTGCA CTTTTCTTT	1366
247	TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCCTCAC CGCTTTCTC	1416
248	CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTCGGG	1466
249	TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TCGGGTGCT	1516
250	CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT	1566
251	TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC	1616
252	TCACTCTGTA GACCAGGCTG GCCTCAAAC TAGAAATCTG CCTGCCTCTG	1666
253	CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG	1716
254	GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT	1766
255	AACTCCCCCTT TTGGCACCTT TCCTTTACAG GACCCCTCC CCCTCCCTGT	1816
256	TTCCCTTCCG GCACCCCTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC	1866
257	CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGTTTCT	1916
258	CCCCCGTTCC CCTTTTTGTT GCCTTTCCCTC CTGGCTCCCC TCCACCTTCC	1966
259	AGCTCACCTT TTTGTTGTT TGTTGTTTG GTTGTGTTGGT TTGCTTTTT	2016
260	TTTTTTTTT GCACCTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC	2066
261	CCTCTGTGTG CCTTTCCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT	2116
262	TCTGCCTTTC CTGCCCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTT	2166
263	CTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTCT GTGCACTTT	2216
264	CCTGACCCCTG CTCCCCCTCC CCTCCCAAGCT CCCCCCTCTT TTCCACCTC	2266
265	CCTTCTCCA GCCTGTCACC CCTCCTCTC TCCTCTCTG TTCTCCCACT	2316

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266	TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCCTC	CTGCCTGCTG	2366
267	GACTTCCTCT	CCAGCCGCC	AGTCCCTGC	AGTCCTGGAG	TCTTCCTGC	2416
268	CTCTCTGTCC	ATCACTCCC	CCTAGTTCA	CTTCCCTTTC	ACTCTCCCT	2466
269	ATGTGTCTCT	CTTCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
270	CCATCACCTC	TCTCCTCCCT	TCCCTTCCCT	CTCTCTTCCA	TTTCTTCCA	2566
271	CCTGCTTCTT	TACCCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCAT	2616
272	TCCATGTCCC	CTCTCAATT	CCTGTCCCCT	TGTGCTCCCT	CACATCTTCC	2666
273	ATTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTCTCT	TGTATCTCCC	2716
274	TCCTCTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATG	CCCTCTACTC	2766
275	TACTTGATCT	TCTCTCTCT	CCACATACCC	TTTTTCTTT	CCACCCCTGCC	2816
276	CTTGTCCCC	AGACCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
277	ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCAAA	ATCAGCAGGA	2916
278	AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
279	AAGTGGCTCC	TATAACCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
280	CTTGATCCTT	GCTGCTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
281	CAGGCCATGTC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
282	GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
283	TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
284	TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTA	3266
285	GGCTAAAGAT	ACTTGGAAC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
286	TTGCTAAAAT	ATTCTTCTC	ACATATTCA	ATTCTCCAG		3355
287	GT	GTT	CCT	GGC	CAT	3396
288	AGG	ATG	ATT	TAT	TTC	3438
289	ATA	CCA	GTG	AAC	CCT	3480
290	AAT	GCT	GAT	GAA	GAG	3522
291	GAG	GAG	GAG	GAG	GAA	3564
292	TTC	TCA	CCT	TAG		3576
293	GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCTAAC	TATGCCTGTA	3626
294	GCTAAGAGCA	TCTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTA	3676
295	TCTTTTACA	TTAATAAGTA	TTAAATTAA	CCAGTATACA	TTTTTAAGAA	3726
296	CCCTAAGTTA	AACAGAAC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
297	GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
298	GACCAAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
299	TTCTTATAGT	ACCTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
300	TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTGTGCG	3976
301	TTCTGATTTT	TTTCATTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
302	CTTAAATTT	CCTTCATCTT	TAATTTCC	TAACTTAGT	TTTTTCACT	4076
303	TAGAATTCAA	TTCAAAATTCT	TAATTCAATC	TTAATTTTA	GATTTCTTAA	4126
304	AATGTTTTT	AAAAAAATG	CAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
305	GTAACTGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
306	GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
307	CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
308	ATAAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
309	ATTTAGTTT	CTCCTTGAGA	AAACATGACA	AGACATAAAA	TTGGCAAGAA	4426
310	AGTCAGGAGT	GTATTCTAAT	AAAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
311	AGTTGCAAAG	CCCAGAAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTT	4526
312	TTTTTCCCC	TTCATTAATT	TTCTAGTTT	TAGTAATCCA	AAAAATTGA	4576
313	TTTGTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
314	GCATGGTGA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
315	AATAAAAGTT	TGACTTGCAT	AC			4698

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318 (2) INFORMATION FOR SEQUENCE ID NO: 6:

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319 (i) SEQUENCE CHARACTERISTICS:
320 (A) LENGTH: 7 amino acids
321 (B) TYPE: amino acid
322 (C) STRANDEDNESS: singular
323 (D) TOPOLOGY: linear
324 (ii) MOLECULE TYPE: protein
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
326
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330 Leu Pro Tyr Leu Gly Trp Leu
331 5
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339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
340 (i) SEQUENCE CHARACTERISTICS:
341 (A) LENGTH: 2419 base pairs
342 (B) TYPE: nucleic acid
343 (C) STRANDEDNESS: singular
344 (D) TOPOLOGY: linear
345 (ii) MOLECULE TYPE: genomic DNA
346 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
347
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351	GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG	50
352	GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC	100
353	TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCCTGAG	150
354	GGCCCGTGGA TTCCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT	200
355	TGGTCTGAGA CAGTATCCTC AGGTACACAGA GCAGAGGATG CACAGGGTGT	250
356	GCCAGCAGTG AATGTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
357	CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT	350
358	CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCTGAGT ACCCTCTCAC	400
359	TTCCCTCTTC AGGTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC	450
360	CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG	500
361	TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT	550
362	CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT	600
363	GCTGCTGCC CTGACGGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC	650
364	ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACAAAGAGGC CCTGGGCTG	700
365	GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC	750
366	CCTGGAGGAG GTGCCCACTG CTGGTCAAC AGATCCTCCC CAGAGTCCTC	800
367	AGGGAGCCTC CGCCTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA	850
368	CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG	900
369	TATCCTGGAG TCCTTGTTC GAGCAGTAAT CACTAAGAAG GTGGCTGATT	950
370	TGGTTGGTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG	1000
371	GCAGAAATGC TGGAGAGTGT CATCAAAAT TACAAGCACT GTTTCCCTGA	1050

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372	GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG	1100
373	TGAAGGAAGC AGACCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA	1150
374	GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC	1200
375	AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG	1250
376	CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT	1300
377	GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA	1350
378	TTTGGTGCAG GAAAAGTACC TGGAGTACCG CAGGTGCCGG ACAGTGATCC	1400
379	CGCACGCTAT GAGTTCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAAGCT	1450
380	ATGTGAAAGT CCTTGAGTAT GTGATCAAGG TCAGTGCAAG AGTCGCTTT	1500
381	TTCTTCCCCT ACCTGCGTGA AGCAGCTTG AGAGAGGAGG AAGAGGGAGT	1550
382	CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC	1600
383	ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG	1650
384	CCCATTCTTC ACTCTGAAGA GAGCGGTCAAG TGTTCTCAGT AGTAGGTTTC	1700
385	TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT	1750
386	TCAAATGTTT TTTTTAAGG GATGGTTGAA TGAACCTCAG CATCCAAGTT	1800
387	TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA	1850
388	GTCTTGTGTT TTATTCAAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG	1900
389	ATAATAACAG CAGTGAATA AGTACTTAAAG AATGTGAAAA ATGAGCAGTA	1950
390	AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTC	2000
391	CTTATACCTC AGTCTATTCT GTAAAATTAA TAAAGATATA TGCACTACCTG	2050
392	GATTCCTTG GCTTCTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG	2100
393	AATTCTTCCT GTTCACTGGC TCTTTCTTC TCCATGCCT GAGCATCTGC	2150
394	TTTTGGAAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT	2200
395	CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG	2250
396	AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAAG AGAGGGGTGA	2300
397	GGGTGTGGGG CTCCGGGTGA GAGTGGTGA GTGTCATGC CCTGAGCTGG	2350
398	GGCATTTTGG GCTTGGAA ACTGCAGTTC CTTCTGGGG AGCTGATTGT	2400
399	AATGATCTTG GGTGGATCC	2419
400		

401 (2) INFORMATION FOR SEQUENCE ID NO: 8:

402 (i) SEQUENCE CHARACTERISTICS:

- 403 (A) LENGTH: 5674 base pairs
- 404 (B) TYPE: nucleic acid
- 405 (C) STRANDEDNESS: singular
- 406 (D) TOPOLOGY: linear

407 (ii) MOLECULE TYPE: genomic DNA

408 (ix) FEATURE:

- 409 (A) NAME/KEY: MAGE-1 gene

410 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

414	CCCGGGGCAC CACTGGCCTC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT	50
415	TACGCCACCC ATCCAAACAT CTCACGCTC ACCCCCAGCC CAAGCCAGGC	100
416	AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAAGCCC AGGTGCCAG	150
417	ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT	200
418	CGGTCTGAGG GGCAGGCTTGA GATCGGGTGA GGGAAAGCGGG CCCAGCTCTG	250
419	TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACCC CACTTACCCCC	300
420	AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCTGG ACCATCTGGT	350
421	GGTGGACTTC TCAGGCTGGG CCACCCCCCAG CCCCCCTTGCT GCTTAAACCA	400
422	CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG	450
423	AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG	500
424	AGGGCTGAGG GTCCCTAAGA CCCCCACTCCC GTGACCCAAC CCCCCACTCCA	550

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425	ATGCTCACTC	CCGTGACCCA	ACCCCTCTT	CATTGTCATT	CCAACCCCCA	600
426	CCCCACATCC	CCCACCCAT	CCCTCAACCC	TGATGCCAT	CCGCCCAGCC	650
427	ATTCCACCTC	CACCCCCACC	CCCACCCCCA	CGCCCACCTC	CACCCCCACC	700
428	CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
429	GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
430	AGGGACGGCG	TAGAGTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
431	AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
432	GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
433	CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCC	CCAGACCCCT	GCTCCAAAAG	1000
434	CCTTGAGAGA	CACCAGGTTC	TTCTCCCCAA	GCTCTGAAT	CAGAGGTTGC	1050
435	TGTGACCAAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
436	GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCC	CCAAGACTGC	1150
437	ACTCCAATCC	CCACTCCCAC	CCCATTGCA	TTCCCATTCC	CCACCCAAACC	1200
438	CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
439	CCTGACCAACC	ACCCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
440	TCACCCCTCAC	TGCCCCCAAC	CCCACCCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
441	CCCATCGCCT	CCCCCATTCT	GGCAGAATCC	GGTTTGC	GGTCTCTCAAC	1400
442	CCAGGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
443	AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
444	ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
445	CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
446	ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
447	GTCTCAGCTG	GACCACCCCC	CGTCCCCTCC	CACTGCCACT	TAACCCACAG	1700
448	GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
449	GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCCGGCAT	TAGGGTCAGG	1800
450	ACCCCTGGGAG	GGAACCTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
451	CACCGCCACC	CCACTCACAT	TCCCATAACCT	ACCCCTTACC	CCCAACCTCA	1900
452	TCTTGTCAAG	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
453	CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAAGGG	2000
454	GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCTAC	TGCGAGATGA	2050
455	GGGAGGCCTC	AGAGGACCCA	GCACCCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
456	ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAC	CAGAACGATG	GGGACTCAGA	2150
457	TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACCGGG	AGGAAGAGGA	2200
458	GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGCCCT	2250
459	GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCCATATTT	CCTGCATCTT	2300
460	TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
461	AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
462	AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
463	CTGTCCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
464	TTCCATTCTC	ACTTGTACCA	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
465	ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
466	GGTTGAGGAA	GCACAGGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
467	AGGCTATTGG	AATCCACACC	CCAGAACCAA	ACGGGTCAGC	CCTGGACACC	2700
468	TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
469	GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
470	TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
471	GAACATGAGG	GAGGACTGAG	GGTACCCCCAG	GACCAGAAC	CTGAGGGAGA	2900
472	CTGCACAGAA	ATCAGCCCTG	CCCCCTGCTGT	CACCCAGAG	ACCATGGGCT	2950
473	GGGCCGTCTG	CCGAGGTCTC	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
474	ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCC	CTCAGGTCAG	TAGAGGGAGC	3050
475	GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCCG	GCACCTCACC	3100
476	CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
477	AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCCTCC	GTCCTTCCAT	3200

478	TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTCTCAG ACCAGCAAA	3250
479	GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC TGCAGTGAAGAA	3300
480	CAGAGGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA GAGTCCAGCC	3350
481	CACCCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC GGTCTGCACC	3400
482	CTGAGGGCCC GTGGATTCCCT CTTCCTGGAG CTCCAGGAAC CAGGCAGTGA	3450
483	GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA GGATGCACAG	3500
484	GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA GGGCCCCACC	3550
485	TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC CTCCCTACTG	3600
486	TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC TGAGTACCC	3650
487	CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC AGAGGACAGG	3700
488	ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAAGATCT GTAAGTAGGC	3750
489	CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC TCTCACACAC	3800
490	TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCAGCT CCTGCCACAC	3850
491	CTCCTGCCCTG CTGCCCTGAC GAGAGTCATC	3880
492	ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG CCT GAG GAA	3922
493	GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG GTG TGT GTG	3964
494	CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC CTG GGC ACC	4006
495	CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT CCT CCC CAG	4048
496	AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC ATC AAC TTC	4090
497	ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC AGC CGT GAA	4132
498	GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG TCC TTG TTC	4174
499	CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG GTT GGT TTT	4216
500	CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC ACA AAG GCA	4258
501	GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG CAC TGT TTT	4300
502	CCT GAG ATC TTC GCC AAA GCC TCT GAG TCC TTG CAG CTG GTC	4342
503	TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC GGC CAC TCC	4384
504	TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT GAT GGC CTG	4426
505	CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC TTC CTG ATA	4468
506	ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC CAT GCT CCT	4510
507	GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG GAG GTG TAT	4552
508	GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG	4594
509	CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC	4636
510	AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG	4678
511	GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA	4711
512	AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC	4750
513	GCTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG	4800
514	GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC	4850
515	AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCTGCC TCGTGTGACA	4900
516	TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC TCAGTAGTAG	4950
517	GTTCCTGTT TATTGGGTGA CTTGGAGATT TATCTTGTT CTCTTTGGA	5000
518	ATTGTTCAA TGTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC	5050
519	AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG	5100
520	TAAGAGTCTT GTGTTTATT CAGATTGGGA AATCCATTCT ATTTTGAA	5150
521	TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAAATGT GAAAAATGAG	5200
522	CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCATT	5250
523	CTTGCCTTAT ACCTCAGTCT ATTCTGAAA ATTTTAAAG ATATATGCAT	5300
524	ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA	5350
525	TAAAAGAATTG TTCCTGTTCA CTGGCTCTT TCTTCCTCCAT GCACGTGAGCA	5400
526	TCTGCTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC	5450
527	AGACTCATAAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT GCAGTCACGT	5500
528	AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG	5550
529	GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA	5600
530	GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCCTCT GGGGGAGCTG	5650

531 ATTGTAATGA TCTTGGGTGG ATCC 5674
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 536 (2) INFORMATION FOR SEQUENCE ID NO: 9:
 537 (i) SEQUENCE CHARACTERISTICS:
 538 (A) LENGTH: 4157 base pairs
 539 (B) TYPE: nucleic acid
 540 (C) STRANDEDNESS: singular
 541 (D) TOPOLOGY: linear
 542 (ii) MOLECULE TYPE: genomic DNA
 543 (ix) FEATURE:
 544 (A) NAME/KEY: MAGE-2 gene
 545 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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 549 CCCATCCAGA TCCCCATCCG GGCAGAAATCC GGTTCCACCC TTGCCGTGAA 50
 550 CCCAGGGAAAG TCACGGGCC GGATGTGACG CCACTGACTT GCACATTGGA 100
 551 GGTCAAGAGGA CAGCGAGATT CTCGCCCTGA GCAACGGCCT GACGTCGGCG 150
 552 GAGGGAAAGCA GGCGCAGGCT CCGTGAGGAG GCAAGGTAAG ACGCCGAGGG 200
 553 AGGACTGAGG CGGGCTCTAC CCCAGACAGA GGGCCCCCAA TTAATCCAGC 250
 554 GCTGCCTCTG CTGCCGGGCC TGGACCACCC TGCAGGGAA GACTTCTCAG 300
 555 GCTCAGTCGC CACCACCTCA CCCCGCCACC CCCCGCCGCT TAAACCGCAG 350
 556 GGAACCTCTGG CGTAAGAGCT TTGTGTGACC AGGGCAGGGC TGGTTAGAAG 400
 557 TGCTCAGGGC CCAGACTCAG CCAGGAATCA AGGTCAAGGAC CCCAAGAGGG 450
 558 GACTGAGGGC AACCCACCCC CTACCCCTCAC TACCAATCCC ATCCCCAAC 500
 559 ACCAAACCCCCA CCCCCATCCC TCAAACACCA ACCCCACCCC CAAACCCCCAT 550
 560 TCCCCATCTCC TCCCCCACCA CCATCCTGGC AGAATCCGGC TTTGCCCTG 600
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 562 ACGTTCACAT GTACGGCTAA GGGAGGGAAAG GGGTTGGTC TCGTGAGTAT 700
 563 GGCCTTTGGG ATGCAGAGGA AGGGCCCAGG CCTCTGGAA GACAGTGGAG 750
 564 TCCTTAGGGG ACCCAGCATG CCAGGACAGG GGGCCCACTG TACCCCTGTC 800
 565 TCAAACGTGAG CCACCTTTTC ATTCAAGCCGA GGGAAATCCTA GGGATGCAGA 850
 566 CCCACTTCAG GGGGTTGGGG CCCAGCCTGC GAGGAGTCAG GGGGAGGAAG 900
 567 AAGAGGGAGG ACTGAGGGGA CCTTGGAGTC CAGATCAGTG GCAACCTTGG 950
 568 GCTGGGGGAT CCTGGGCACA GTGGCCGAAT GTGCCCGTG CTCATTGCAC 1000
 569 CTTCAAGGTG ACAGAGAGTT GAGGGCTGTG GTCTGAGGGC TGGGACTTCA 1050
 570 GGTCAAGCAGA GGGAGGAATC CCAGGATCTG CCGGACCCAA GGTGTGCC 1100
 571 CTTCATGAGG ACTCCCCATA CCCCCGGCCC AGAAAAGAAGG GATGCCACAG 1150
 572 AGTCTGGAAG TAAATTGTTT TTAGCTCTGG GGGAAACCTGA TCAGGGATGG 1200
 573 CCCTAAGTGA CAATCTCATT TGTACCACAG GCAGGAGGTT GGGGAACCC 1250
 574 CAGGGAGATA AGGTGTTGGT GTAAAGAGGA GCTGTCTGCT CATTTCAGGG 1300
 575 GGTTCCCCCT TGAGAAAGGG CAGTCCCTGG CAGGAGTAAA GATGAGTAAC 1350
 576 CCACAGGAGG CCATCATAAC GTTCACCCCTA GAACCAAAGG GGTCAAGCC 1400
 577 GGACAACGCA CGTGGGGTAA CAGGATGTGG CCCCTCCTCA CTTGTCTTC 1450
 578 CAGATCTCAG GGAGTTGATG ACCTTGTGTTT CAGAAGGTGA CTCAGTCAC 1500
 579 ACAGGGGCCCT CTCTGGTCGA CAGATGCAGT GGTTCTAGGA TCTGCCAAGC 1550
 580 ATCCAGGTGG AGAGCCTGAG GTAGGATTGA GGGTACCCCT GGGCCAGAAT 1600
 581 GCAGCAAGGG GGCCCCATAG AAATCTGCC TGCCCCCTGCG GTTACTTCAG 1650
 582 AGACCCCTGGG CAGGGCTGTC AGCTGAAGTC CCTCCATTAT CTGGGATCTT 1700
 583 TGATGTCAGG GAAGGGAGG CCTTGGTCTG AAGGGCTGG AGTCAGGTCA 1750

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584	GTAGAGGGAG GGTCTCAGGC CCTGCCAGGA GTGGACGTGA GGACCAAGCG	1800
585	GACTCGTCAC CCAGGACACC TGGACTCCAA TGAATTGAC ATCTCTCGTT	1850
586	GTCCTTCGCG GAGGACCTGG TCACGTATGG CCAGATGTGG GTCCCCCTCTA	1900
587	TCTCCTTCTG TACCATATCA GGGATGTGAG TTCTTGACAT GAGAGATTCT	1950
588	CAAGCCAGCA AAAGGGTGGG ATTAGGCCCT ACAAGGAGAA AGGTGAGGGC	2000
589	CCTGAGTGAG CACAGAGGGG ACCCTCCACC CAAGTAGAGT GGGGACCTCA	2050
590	CGGAGTCTGG CCAACCCCTGC TGAGACTTCT GGGAAATCCGT GGCTGTGCTT	2100
591	GCAGTCTGCA CACTGAAGGC CCGTGCATTC CTCTCCCAGG AATCAGGAGC	2150
592	TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC CTCAGGTAC	2200
593	AGAGCAGAGG GGACGCAGAC AGTGCCAACA CTGAAGGTTT GCCTGGAATG	2250
594	CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCCTG	2300
595	GCCTCACCCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG	2350
596	CTGTACCCCTG AGGTGCCCTC CCACTTCCCTC CTTCAGGTT TCAGGGGGAC	2400
597	AGGCTGACAA GTAGGACCCG AGGCAGTGGG GGAGCATTGA AGGAGAAGAT	2450
598	CTGTAAGTAA GCCTTGTCA GAGCCTCCAA GGTTCAAGTTC AGTTCTCACC	2500
599	TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG	2550
600	CCCAGCTCCT GCCCCCACTC CTGCCTGCTG CCCTGACCAG AGTCATC	2597
601	ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	2639
602	GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	2681
603	CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT	2723
604	TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC	2765
605	GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC	2807
606	TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT	2849
607	GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATG TTT	2891
608	CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG	2933
609	ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	2975
610	AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC	3017
611	AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC	3059
612	TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA	3101
613	GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG	3143
614	GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG	3185
615	CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	3227
616	ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	3269
617	CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GAC AGT GTC	3311
618	TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG	3353
619	GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT	3395
620	GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA	3437
621	ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT	3479
622	GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT	3521
623	TTG AGA GAG GGA GAA GAG TGA	3542
624	GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	3592
625	GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCCTCG TGTGATATGA	3642
626	GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG	3692
627	TTTCTGTTCT GTTGGATGAC TTGAGATT ATCTTTCTTT CCTGTTGGAA	3742
628	TTGTTCAAAT GTTCTTTA ACAAAATGGTT GGATGAACCT CAGCATCCAA	3792
629	GTGTTATGAAT GACAGTAGTC ACACATAGTG CTGTTATAT AGTTTAGGGG	3842
630	TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGAG	3892
631	TTGTCACATA ATAACAGCAG TGGAAATATGT ATTTGCCAT ATTGTGAACG	3942
632	AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT	3992
633	TGCCTTATAC CTCAGTCTAT TATGAAAAAT TAAAAATATG TGTATGTTT	4042
634	TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT	4092
635	TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC	4142
636	CCTGGTAGTA GTGGG	4157

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642 (2) INFORMATION FOR SEQUENCE ID NO: 10:
643 (i) SEQUENCE CHARACTERISTICS:
644 (A) LENGTH: 662 base pairs
645 (B) TYPE: nucleic acid
646 (C) STRANDEDNESS: singular
647 (D) TOPOLOGY: linear
648 (ii) MOLECULE TYPE: genomic DNA
649 (ix) FEATURE:
650 (A) NAME/KEY: MAGE-21 gene
651 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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655 GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
656 AGGGAAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
657 CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
658 GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
659 ACTGAGGCAGG	GCCTCACCCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
660 CCTCTGCTGC	CAGGCCTGGA	CCACCCCTGCA	GGGGAAAGACT	TCTCAGGCTC	300
661 AGTCGCCACC	ACCTCACCCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
662 CTCTGGTGTA	AGAGCTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
663 CAGGGCCCGAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCCA	AGAGGGGACT	450
664 GAGGGTAACC	CCCCCGCACC	CCACCCACCA	TTCCCATCCC	CCAACACCAA	500
665 CCCCACCCCC	ATCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
666 ACGGCACCCCC	CAAACCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
667 GAGCTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGAA	TGGCGGCCAA	650
668 GCACGCGGAT	CC				662

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678 (2) INFORMATION FOR SEQUENCE ID NO: 11:
679 (i) SEQUENCE CHARACTERISTICS:
680 (A) LENGTH: 1640 base pairs
681 (B) TYPE: nucleic acid
682 (C) STRANDEDNESS: singular
683 (D) TOPOLOGY: linear
684 (ii) MOLECULE TYPE: cDNA to mRNA
685 (ix) FEATURE:
686 (A) NAME/KEY: cDNA MAGE-3
687 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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691 GCCCGGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG 50
692 GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA 100
693 AGATCTGCCA GTGGGTCTCC ATTGCCAGC TCCTGCCAC ACTCCCGCCT 150
694 GTTGCCCTGA CCAGAGTCAT C 171
695 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 213
696 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 255
697 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 297
698 TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 339
699 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
700 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
701 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
702 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
703 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
704 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
705 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
706 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
707 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
708 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
709 CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 801
710 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
711 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
712 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
713 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
714 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
715 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
716 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
717 TTG AGA GAG GGG GAA GAG TGA 1116
718 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
719 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCCTC TGTGACGTGA 1216
720 GGCCCATTCT TCACTCTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
721 TTTCTGTTCT GTTGGATGAC TTGAGATTA TTCTTGTGTT CCTGTTGGAG 1316
722 TTGTTCAAAT GTTCCCTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
723 GTTATGAAT GACAGTAGTC ACACATAGTG CTGTTATAT AGTTTAGGAG 1416
724 TAAGAGTCTT GttTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
725 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
726 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
727 ATTCTTGCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
728 ACCAGGATT CTTGACTTC TTTG 1640
729
730
731
732

733 (2) INFORMATION FOR SEQUENCE ID NO: 12:

734 (i) SEQUENCE CHARACTERISTICS:
735 (A) LENGTH: 943 base pairs
736 (B) TYPE: nucleic acid
737 (C) STRANDEDNESS: singular
738 (D) TOPOLOGY: linear
739 (ii) MOLECULE TYPE: genomic DNA
740 (ix) FEATURE:
741 (A) NAME/KEY: MAGE-31 gene
742 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

743
 744
 745
 746 GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50
 747 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
 748 GCCCGTGGAT TCCTCTCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
 749 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGGgCTCA 200
 750 GATA GTGCCA ACGGTGAAGG TTTCGCTTGG ATTCAAACCA AGGGCCCCAC 250
 751 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
 752 TTCAGTCCTG CAGCCTCAGC ATGCCTGGC CGGATGTACC CTGAGGTGCC 350
 753 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400
 754 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTG 450
 755 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500
 756 TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCACCA 550
 757 CTCCCGCCTG TTGCCCTGAC CAGAGTCATC 580
 758 ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 622
 759 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 664
 760 CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT 706
 761 TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC 748
 762 GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 790
 763 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 832
 764 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 874
 765 CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG 916
 766 GTG GCC AAG TTG GTT CAT TTT CTG CTC 943
 767
 768
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 771 (2) INFORMATION FOR SEQUENCE ID NO: 13:
 772 (i) SEQUENCE CHARACTERISTICS:
 773 (A) LENGTH: 1067 base pairs
 774 (B) TYPE: nucleic acid
 775 (C) STRANDEDNESS: singular
 776 (D) TOPOLOGY: linear
 777 (ii) MOLECULE TYPE: cDNA to mRNA
 778 (ix) FEATURE:
 779 (A) NAME/KEY: cDNA MAGE-4
 780 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 781
 782
 783
 784 GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA 39
 785 GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG 81
 786 CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA 123
 787 ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT 165
 788 GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT 207
 789 GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC 249
 790 ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG 291
 791 GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC 333
 792 GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG 375
 793 GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT 417
 794 GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC 459
 795 ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG 501

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796	GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	543
797	CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	585
798	CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	627
799	TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	669
800	TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGCAGG GCTGGCCAG	719
801	TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	769
802	GCCCCATTCTT CACTCTGTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG	819
803	GTTCCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTACA	869
804	ATTGTTGAAA TGTTCCCTTT AATGGATGGT TGAATTAAC TCAAGCATCCA	919
805	AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	969
806	AAGAGTCTTG TTTTTTATTG AGATTGGAA ATCCGTTCTA TTTTGTGAAT	1019
807	TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1067
808		
809		

810 (2) INFORMATION FOR SEQUENCE ID NO: 14:

811	(i) SEQUENCE CHARACTERISTICS:	
812	(A) LENGTH: 226 base pairs	
813	(B) TYPE: nucleic acid	
814	(C) STRANDEDNESS: singular	
815	(D) TOPOLOGY: linear	
816	(ii) MOLECULE TYPE: genomic DNA	
817	(ix) FEATURE:	
818	(A) NAME/KEY: MAGE-5 gene	
819	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
820		
821		
822		

823	AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT	50
824	AAGCCTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA GGCTTCTCAC	100
825	ATGCTCCCTC TCTCTCCAGG CCAGTGGTC TCCATTGCC AGCTCCTGCC	150
826	CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	184
827	ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	226
828		

829 (2) INFORMATION FOR SEQUENCE ID NO: 15:

830	(i) SEQUENCE CHARACTERISTICS:	
831	(A) LENGTH: 225 base pairs	
832	(B) TYPE: nucleic acid	
833	(C) STRANDEDNESS: singular	
834	(D) TOPOLOGY: linear	
835	(ii) MOLECULE TYPE: cDNA	
836	(ix) FEATURE:	
837	(A) NAME/KEY: MAGE-6 gene	
838	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
839		
840		
841		

842	TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG	42
843	CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC	84
844	GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC	126
845	GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC	168
846	TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC	210
847	TGT GCC CCT GAG GAG	225
848		

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853 (2) INFORMATION FOR SEQUENCE ID NO: 16:
854 (i) SEQUENCE CHARACTERISTICS:
855 (A) LENGTH: 166 base pairs
856 (B) TYPE: nucleic acid
857 (C) STRANDEDNESS: singular
858 (D) TOPOLOGY: linear
859 (ii) MOLECULE TYPE: genomic DNA
860 (ix) FEATURE:
861 (A) NAME/KEY: MAGE-7 gene
862 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

863
864
865

866	ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG	42
867	TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC	84
868	CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC	126
869	TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A	166
870		

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/807,043B

DATE: 11/06/92
TIME: 14:38:15

LINE ERROR

ORIGINAL TEXT

24 Wrong application Serial Number

(A) APPLICATION NUMBER: 07/807,043



PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/807,043B

DATE: 11/06/92
TIME: 14:38:15

MANDATORY IDENTIFIER THAT WAS NOT FOUND

COUNTRY

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/807,043B

DATE: 11/06/92
TIME: 14:38:15

LINE ORIGINAL TEXT

3 (1) APPLICANTS: Boon, Thierry, Van den
50 (2) INFORMATION FOR SEQUENCE ID NO: 1:
72 (2) INFORMATION FOR SEQUENCE ID NO: 2:
140 (2) INFORMATION FOR SEQUENCE ID NO: 3:
159 (2) INFORMATION FOR SEQUENCE ID NO: 4:
206 (2) INFORMATION FOR SEQUENCE ID NO: 5:
318 (2) INFORMATION FOR SEQUENCE ID NO: 6:
339 (2) INFORMATION FOR SEQUENCE ID NO: 7:
401 (2) INFORMATION FOR SEQUENCE ID NO: 8:
536 (2) INFORMATION FOR SEQUENCE ID NO: 9:
642 (2) INFORMATION FOR SEQUENCE ID NO: 10:
678 (2) INFORMATION FOR SEQUENCE ID NO: 11:
733 (2) INFORMATION FOR SEQUENCE ID NO: 12:
771 (2) INFORMATION FOR SEQUENCE ID NO: 13:
810 (2) INFORMATION FOR SEQUENCE ID NO: 14:
829 (2) INFORMATION FOR SEQUENCE ID NO: 15:
853 (2) INFORMATION FOR SEQUENCE ID NO: 16:

CORRECTED TEXT

(1) APPLICANT: Boon, Thierry, Van den E
(2) INFORMATION FOR SEQ ID NO: 1:
(2) INFORMATION FOR SEQ ID NO: 2:
(2) INFORMATION FOR SEQ ID NO: 3:
(2) INFORMATION FOR SEQ ID NO: 4:
(2) INFORMATION FOR SEQ ID NO: 5:
(2) INFORMATION FOR SEQ ID NO: 6:
(2) INFORMATION FOR SEQ ID NO: 7:
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(2) INFORMATION FOR SEQ ID NO: 13:
(2) INFORMATION FOR SEQ ID NO: 14:
(2) INFORMATION FOR SEQ ID NO: 15:
(2) INFORMATION FOR SEQ ID NO: 16: